

What is claimed is:

1. A method of identifying an immunodominant epitope of an antigen comprising:
 - examining amino acid sequences within the antigen for binding affinity to an MHC molecule;
 - examining amino acid sequences within the antigen to determine sequence similarity to the host proteome; and
 - selecting an amino acid sequence within the antigen having high MHC binding affinity and low sequence similarity to the host proteome.
2. The method of Claim 1, wherein the MHC molecule is a class I MHC molecule.
3. The method of Claim 1, wherein the MHC molecule is a class II MHC molecule.
4. The method of Claim 1, wherein binding affinity is predicted by comparing amino acid sequences within the antigen to a consensus MHC binding sequence.
5. The method of Claim 1, wherein sequence similarity is examined by comparing overlapping amino acid sequences within the antigen to the host proteome.
6. The method of Claim 5, wherein the overlapping amino acid sequences are 4 to 10 amino acids in length.
7. The method of Claim 5, wherein the overlapping amino acid sequences are 5, 6, or 7 amino acids in length.
8. The method of Claim 5, wherein the short overlapping amino acid sequences are offset by 5 amino acids.

9. The method of Claim 5, wherein the short overlapping amino acid sequences are offset by 1 or 2 amino acids.

10. A method of producing a polypeptide useful for eliciting an immune response against an antigen in a host comprising;

(a) analyzing amino acid sequences within the antigen for binding affinity to an MHC molecule;

(b) examining amino acid sequences within the antigen to determine sequence similarity to the host proteome;

(c) selecting an amino acid sequence having high MHC binding affinity and low sequence similarity; and

(d) producing a polypeptide comprising the selected amino acid sequence.

11. The method of Claim 10, wherein binding affinity is predicted by comparing amino acid sequences within the antigen to a consensus MHC binding sequence.

12. The method of Claim 10, wherein sequence similarity is examined by comparing short overlapping amino acid sequences within the antigen to the host proteome.

13. A method of eliciting a therapeutic immune response to an antigen comprising administering to a subject an effective amount a polypeptide comprising an amino acid selected by:

(a) analyzing amino acid sequences within the antigen for binding affinity to an MHC molecule;

(b) examining amino acid sequences within the antigen to determine sequence similarity to the host proteome; and

(c) selecting an amino acid sequence having high MHC binding affinity and low sequence similarity.

14. The method of Claim 13, wherein the MHC molecule is a class II MHC molecule and the therapeutic response is a humoral response.

15. The method of Claim 13, wherein the selected amino acid sequence comprises a B cell epitope.
16. The method of Claim 13, wherein the polypeptide further comprises a B cell epitope linked to the selected amino acid sequence.
17. The method of Claim 13, wherein the MHC molecule is a class I MHC molecule and the therapeutic response is a cytotoxic cellular response.
18. The method of Claim 13, wherein the antigen is a tumor antigen.
19. The method of Claim 13 wherein the antigen is from an infectious agent.